IN THE CLAIMS:

1-13. (cancelled)

14. (currently amended) A method of ~~genotyping a~~ determining the genotype of a bioagent comprising the steps of:

~~determining a first molecular mass of a first amplification product of a first bioagent identifying amplicon that contains genotyping information; and~~

~~comparing the first molecular mass to a second molecular mass of a second bioagent identifying amplicon that contains genotyping information, wherein the first and second bioagent identifying amplicons are correlative, and wherein a match between the first molecular mass and the second molecular mass identifies a genotype of the bioagent.~~

selecting at least one pair of oligonucleotide primers, wherein one member of said pair of primers hybridizes to a first conserved region of nucleic acid encoding ribosomal RNA and the other member of said pair of primers hybridizes to a second conserved region of nucleic acid encoding ribosomal RNA wherein said first and second conserved regions flank a variable nucleic acid region which varies among bioagents;

amplifying nucleic acid from said bioagent with said pair of oligonucleotide primers to produce an amplification product;

determining the molecular mass of said amplification product by mass spectrometry;

calculating the base composition of said amplification product from said molecular mass;

comparing said base composition to calculated or measured base compositions of amplification products of known bioagents produced by using said pair of oligonucleotide primers, thereby identifying said unknown bioagent at the species level; and

identifying a sub-species characteristic of said bioagent, thereby thereby determining the genotype of said bioagent.

15. (currently amended) The method of claim 14 wherein the ~~genotyping information~~ sub-species characteristic comprises a single nucleotide polymorphism.

16. (currently amended) The method of claim 14 wherein the ~~genotyping information~~ sub-species characteristic comprises a variable number tandem repeat (VNTR).

17. (currently amended) The method of claim 14 wherein the ~~genotyping information~~ sub-species characteristic comprises a pathogenicity factor.

18. (previously presented) The method of claim 17 wherein the pathogenicity factor is a pathogenicity island, a virulence marker, or a toxin component.

19. (currently amended) The method of claim 18 ~~which is used to detect a~~ wherein said toxin gene has been inserted by genetic engineering.

20-28. (cancelled)

29. (new) The method of claim 1 wherein the molecular masses of said first and second amplification products are determined by ESI-TOF mass spectrometry.

30. (new) The method of claim 1 wherein the bioagent is a bacterium, mold, fungus or parasite.

31. (new) The method of determining the genotype of a bioagent comprising the steps of:

selecting at least one pair of oligonucleotide primers, wherein one member of said pair of primers hybridizes to a first conserved region of nucleic acid encoding a protein that participates in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity, and the other member of said pair of primers hybridizes to a second conserved region of nucleic acid encoding a protein that participates in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity, wherein said first and second conserved regions flank a variable nucleic acid region which varies among bioagents;

amplifying nucleic acid from said bioagent with said pair of oligonucleotide primers to produce an amplification product;

determining the molecular mass of said amplification product by mass spectrometry;

calculating the base composition of said amplification product from said molecular mass;

comparing said base composition to calculated or measured base compositions of amplification products of known bioagents produced by using said pair of oligonucleotide primers, thereby identifying said unknown bioagent at the species level; and

identifying a sub-species characteristic of said bioagent, thereby thereby determining the genotype of said bioagent.

32. (new) The method of claim 31 wherein said sub-species characteristic comprises a single nucleotide polymorphism.

33. (new) The method of claim 31 wherein said sub-species characteristic comprises a variable number tandem repeat (VNTR).

34. (new) The method of claim 31 wherein said sub-species characteristic comprises a pathogenicity factor.

35. (new) The method of claim 34 wherein said pathogenicity factor is a pathogenicity island, a virulence marker, or a toxin gene.

36. (new) The method of claim 35 wherein said toxin gene has been inserted by genetic engineering.

37. (new) The method of claim 31 wherein said molecular masses of said first and second amplification products are determined by ESI-TOF mass spectrometry.

38. (new) A method of claim 31 wherein the bioagent is a bacterium, virus, mold, fungus or parasite.